

5' AGC AAG CAG GTA AAC GAG GAG CTT TGT ACA AAC ACA CAC CAC AGA CCA ACA CAT CCG GGG 56

ATG GCT GTG TGT TGC TAG TGC AGC AGA GGC TGA TTA AAC ACT CAG TGT GTT GGC TCT 110

CTG TGC CAC TCC TGG AAA ATA ATG AAT TGG GTA AGG AAC AGT TAA TAA GAA AAT 164

GTG CCT TGC TAA CTG TGC ACA TTA CAA CAA AGA GCT GGC AGC TCC TGA AGG AAA 218

AGG GCT TGT GCC GCT GCC GTT CAA ACT TGT CAG TCA ACT CAT CAT GCC AGC AGC CTC 272

AGC GTC TGC CTC CCC AGC ACA CCC TCA TTA CAT CAT GTG TCT GTC TGG CCT GAT CTG 326

TGC ATC TGC TCG GAG ACG CTC CTC CTG ACA AGT CGG GAA TTT CTC CTC TAT TTC TCC ACT 380

FIGURE 1A

GGT	GCA	AAG	AGC	AGC	GGA	TTT	CTC	CCT	GCT	TCT	CTT	CTG	TCA	CCC	CCG	CTC	CTC	TCC
434	389	398	407	416	425	434												
CCC	AGG	AGG	CTC	CTT	GAT	452	TTA	TGG	TAG	CTT	TGG	ACT	TGC	TTC	CCC	GTC	TGA	CTG
443	443	452	461	470	479	488												
TCC	TTG	ACT	TCT	AGA	ATG	506	GAA	GAA	GCT	GAG	CTG	GTG	AAG	GGA	AGA	CTC	CAG	GCC
542	497	506	515	524	533	542												
I	T	D	K	R	K	I	E	E	A	E	L	V	K	G	R	L	Q	A
596	551	560	569	578	587	596												
ATC	ACA	GAT	AAA	AGA	AAA	ATA	CAG	GAA	GAA	GAA	ATC	TCA	CAG	AAG	CGT	CTG	AAA	ATA
650	605	614	623	632	641	650												
GAG	GAA	GAC	AAA	CTA	AAG	CAC	CAG	CAG	CAT	TTG	AAG	AAA	AAG	GCC	TTG	AGG	GAG	AAA
704	659	668	677	686	695	704												
TGG	CTT	CTA	GAT	GGA	ATC	AGC	AGC	AGC	GGA	AAA	GAA	CAG	GAA	GAG	ATG	AAG	AAG	CAA
Q	W	L	L	D	G	I	S	S	G	K	E	Q	E	E	M	K	K	Q

2 of 21

AAT	CAA	CAA	GAC	CAG	CAC	CAG	ATC	CAG	GTT	CTA	GAA	CAA	AGT	ATC	CTC	AGG	CTT
N	Q	Q	D	Q	H	Q	I	Q	V	L	E	Q	S	I	L	R	L
GAG	AAA	GAG	ATC	CAA	GAT	CTT	GAA	AAA	GCT	GAA	CTG	CAA	ATC	TCA	ACG	AAG	GAA
E	K	E	I	Q	D	L	E	K	A	E	L	Q	I	S	T	K	E
GAG	GCC	ATT	TTA	AAG	AAA	CTA	AAG	TCA	ATT	GAG	CGG	ACA	ACA	GAA	GAC	ATT	ATA
E	A	I	L	K	K	L	K	S	I	E	R	T	T	E	D	I	I
AGA	TCT	GTG	AAA	GTG	GAA	AGA	GAA	GAA	AGA	GCA	GAA	GAG	TCA	ATT	GAG	GAC	ATC
R	S	V	K	V	E	R	E	E	R	A	E	E	S	I	E	D	I
TAT	GCT	AAT	ATC	CCT	GAC	CTT	CCA	AAG	TCC	TAC	ATA	CCT	TCT	AGG	TTA	AGG	AAG
Y	A	N	I	P	D	L	P	K	S	Y	I	P	S	R	L	R	K
GAG	ATA	AAT	GAA	GAA	AAA	GAA	GAT	GAT	GAA	CAA	AAT	AGG	AAA	GCT	TTA	TAT	GCC
E	I	N	E	E	K	E	D	D	E	Q	N	R	K	A	L	Y	A

3 of 21

1037 1046 1055 1064 1073 1082  
ATG GAA ATT AAA GTT GAA AAA GAC TTG AAG ACT GGA GAA AGT ACA GTT CTG TCT  
M E I K V E K D L K T G E S T V L S  
1091 1100 1109 1118 1127 1136  
TCA ATA CCT CTG CCA TCA GAT GAC TTT AAA GGT ACA GGA ATA AAA GTT TAT GAT  
S I P L P S D D F K G T G I K V Y D  
1145 1154 1163 1172 1181 1190  
GAT GGG CAA AAG TCA GTG TAT GCA GTA AGT TCT AAT CAC AGT GCA GCA TAC AAT  
D G Q K S V Y A V S S N H S A A Y N  
1199 1208 1217 1226 1235 1244  
GGC ACC GAT GGC CTG GCA CCA CCA GTT GAA GTA GAG GAA CTT CTA AGA CAA GCC TCA  
G T D G L A P V E V E E L L R Q A S  
1253 1262 1271 1280 1289 1298  
GAG AGA AAC TCT AAA TCC CCA ACA GAG TAT CAT GAG CCT GAT GTA TAT GCC AAT CCC  
E R N S K S P T E Y H E P V Y A N P  
1307 1316 1325 1334 1343 1352  
TTT TAC AGG CCT ACA ACC CCA CAG AGA GAA ACG GTG ACC CCT GGA CCA AAC TTT  
F Y R P T T P Q R E T V T P G P N F

FIGURE 1D

1361 1370 1379 1388 1397 1406  
CAA GAA AGG ATA AAG ATT AAA ACT AAT GGA CTG GGT ATT GGT GTA AAT GAA TCC  
Q E R I K I K T N G L G I G V N E S  
1415 1424 1433 1442 1451 1460  
ATA CAC AAT ATG GGC AAT GGT CTT TCA GAG GAA AGG GGA AAC AAC TTC AAT CAC  
I H N M G N G L S E E R G N N F N H  
1469 1478 1487 1496 1505 1514  
ATC AGT CCC ATT CCG CCA GTG CCT CAT CCC CGA TCA GTG ATT CAA CAA GCA GAA  
I S P I P P V P H P R S V I Q Q A E  
1523 1532 1541 1550 1559 1568  
GAG AAG CTT CAC ACC CCG CAA AAA AGG CTA ATG ACT CCT TGG GAA GAA TCG AAT  
E K L H T P P Q K R L M T P W E S N  
1577 1586 1595 1604 1613 1622  
GTC ATG CAG GAC AAA GAT GCA CCC TCT CCA AAG CCA AGG CTG AGC CCC AGA GAG  
V M Q D K D A P S P K P R L S P R E  
1631 1640 1649 1658 1667 1676  
ACA ATA TTT GGG AAA TCT GAA CAC CAG AAT TCT TCA CCC ACT TGT CAG GAG GAC  
T I F G K S E H Q N S S P T C Q E D

FIGURE 1E

1685	1694	1703	1712	1721	1730
GAG GAA GAT GTC AGA TAT AAT ATC GTT CAT TCC CTG CCT CCA GAC ATA AAT GAT					
E E D V R Y N I V H S L P P D I N D					
1739	1748	1757	1766	1775	1784
ACA GAA CCG GTG ACA ATG ATT TTC ATG GGG TAT CAG CAG GCA GAA GAC AGT GAA					
T E P V T M I F M G Y Q Q A E D S E					
1793	1802	1811	1820	1829	1838
GAA GAT AAG AAG TTT CTG ACA GGA TAT GAT GGG ATC ATC CAT GCT GAG CTG GTT					
E D K K F L T G Y D G I I H A E L V					
1847	1856	1865	1874	1883	1892
GTG ATT GAT GAT GAG GAG GAT GAG GAA GGA GAA GCA GAG AAA CCG TCC TAC					
V I D D E E E D E G E A E K P S Y					
1901	1910	1919	1928	1937	1946
CAC CCC ATA GCT CCC CAT AGT CAG GTG TAC CAG CCA GCC AAA CCA ACA CCA CTT					
H P I A P H S Q V Y Q P A K P T P L					
1955	1964	1973	1982	1991	2000
CCT AGA AAA AGA TCA GAA GCT AGT CCT CAT GAA AAC ACA AAT CAT AAA TCC CCC					
P R K R S E A S P H E N T N H K S P					

FIGURE 1F

6821

2009			2018			2027			2036			2045			2054		
CAC	AAA	AAT	TCC	ATA	TCT	CTG	AAA	GAG	CAA	GAA	GAA	AGC	TTA	GGC	AGC	CCT	GTC
H	K	N	S	I	S	L	K	E	Q	E	E	S	L	G	S	P	V
2063			2072			2081			2090			2099			2108		
CAC	CAT	TCC	CCA	TTT	GAT	GCT	CAG	ACA	ACT	GGA	GAT	GGG	ACT	GAG	GAT	CCA	TCC
H	H	S	P	F	D	A	Q	T	T	G	D	G	T	E	D	P	S
2117			2126			2135			2144			2153			2162		
TTA	ACA	GCT	TTA	AGG	ATG	AGA	ATG	GCA	AAG	CTG	GGA	AAA	AAG	GTG	ATC	TAA	GAG
L	T	A	L	R	M	R	M	A	K	L	G	K	K	V	I	*	
2171			2180			2189			2198			2207			2216		
TTG	TAC	CAC	CTA	TAT	AAA	CAT	CCT	TTG	AAG	AAG	AAA	CTA	AGA	AGC	ATT	TGC	AAA
2225			2234			2243			2252			2261			2270		
TTT	CTC	TTC	TGG	ATA	TTT	TGT	TTA	TTT	TTT	CTG	AAG	TCC	AAA	AAA	TTA	TCA	TTA
2279			2288			2297			2306			2315			2324		
CAG	TGT	ACC	ATA	TTA	AGC	CAT	GTG	AAT	AAG	TAG	TAG	TCA	TTA	TTT	GTG	AAA	AAT

FIGURE 1G

7821

2333	2342	2351	2360	2369	2378
TCC CAA AAA	GCT GGG GAA AAC AAA	TGT GTA ACT TTT	CCA GTT ACT	TGA CAC	GAT
---	---	---	---	---	---
2387	2396	2405	2414	2423	2432
TCA GTG GGG	GAA AAC CAG CAT TTT	TTA TTC TAT TGA	TAC CAA AGC	ATT TCT	AAT
---	---	---	---	---	---
2441	2450	2459	2468	2477	
AAG AGC TTG	TTA AAT TTA AGA ATA AAG	TTA TTT AAA	ATA AAA AAA	AAA A 3'	
---	---	---	---	---	---

FIGURE 1H



5' 3' 1' 2' 4' 6' 8' 10' 12' 14' 16' 18' 20' 22' 24' 26' 28' 30' 32' 34' 36' 38' 40' 42' 44' 46' 48' 50' 52' 54' 56' 58' 60' 62' 64' 66' 68' 70' 72' 74' 76' 78' 80' 82' 84' 86' 88' 90' 92' 94' 96' 98' 100'

11	GTA	TCC	CTT	GTT	TAA	TCA	CTT	TTG	TGG	TTA	AAA	GAG	ACC	TTT	GGG	TCA	GTC	TGC	56
65	CTC	ATT	CCT	TGA	AGA	GTT	TAG	CCC	TGG	CTC	ACT	TTT	CAC	TCT	ATT	TCT	TCT	CCT	110
119	GTC	TCA	AGA	AAG	AAA	AAA	AAA	AGA	GAC	AAA	TTA	CCC	AGA	AAC	CCC	TCC	CTT	CCC	164
173	CAC	ATG	GAG	GCC	TTG	GCA	AAT	GTT	AAT	TTT	CCT	AGA	AAA	TCC	TTC	AGA	CCT	GAA	218
227	GAC	GCA	GGA	AAA	GAA	TCT	GGC	TCT	CAG	GGT	GGC	TTT	TGC	GTC	CCC	GCC	GCC	AGG	272
281	CCC	CAG	ACT	ATG	GTC	ACA	GGG	CCG	TCC	TGT	TCC	TCC	CCG	GGA	CTC	CAG	AAT	TTC	326
	P	Q	T	M	V	T	G	P	S	C	S	S	P	G	L	Q	N	F	

FIGURE 2A

TCT	335	CAA	AGG	AAA	GAA	344	AAC	AGG	GCA	353	TGC	GCT	TGT	362	TGG	CAA	AAC	371	GCA	GGG	380
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	P	Q	R	K	E		N	R	A		C	A	C		W	Q	N		A	G	P
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
GCT	389	AAA	AAC	CCC	ATG	398	TGT	GTA	CGA	407	TTA	AAA	GTT	416	GGC	CGT	CCC		CAG	GCC	434
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				TCC
A	P	K	N	P	M		C	V	R		L	K	V		G	R	P		Q	A	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
CAG	443	AAA	CTT	AAA	GAG	452	ACA	GGG	CTT	461	TGC	TGA	AAA	470	CCA	AAC	ATG	GGC	CAG	CTG	488
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
Q	R	K	L	K	E		T	G	L		C	*									
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
GGC	497	TTA	ACA	ACC	TAG	506	AGA	CTT	TCC	515	GGA	GCT	GCC	524	TGG	AAC	AGA	GCC	TGC	GGG	542
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
AAA	551	GGC	TTG	CCA	GAG	560	ACA	CTC	ACA	569	GTT	TCC	TTC	578	ATG	GCC	TGT	TTT	GGT	CCC	596
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
CTA	605	ATC	TCC	ACA	TCA	614	TTG	TCT	TTC	623	TTG	TGC	CTT	632	TTC	CTT	GGT	GAG	CAA	CAG	650
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
AAA	659	AAG	GGT	TCC	AAG	668	CCT	CTA	AAA	677	ATG	TGC	TTT	686	GTG	ATC	AGG	AGT	GCG	CTC	704

FIGURE 2B

10 y 21

713	722	731	740	749	758
CAA ACC AAA	TAC GCG CGC	TGC CCT TTC	GAG GCC AGT	GAG CTC AGC	CTC CAA GGC
---	---	---	---	---	---
767	776	785	794	803	812
TTT AAA GCC	ACA TTT CAG	CAA GAG AAA	GCG CTG AGA	GCT CGC AGG	TTC ATT AAA
---	---	---	---	---	---
821	830	839	848	857	866
GAA GGC AAA	GCA CTG GTT	TCT CTC CTT	AGA AAA GTA	GGT TTC TTG	GCT TGA TGT
---	---	---	---	---	---
875	884	893	902	911	920
AGA CTG GCT	TGC TTT GAT	TTT TAG TGA	AGG GAA TGT	ACG TAA AAC	AAA ATA GGG
---	---	---	---	---	---
929	938	947	956	965	974
CTT GGC TGG	TCA AAG GAG	ACA AGC AGG	ATG GAT GGA	TGG ATG GAT	GGA TGG ATG
---	---	---	---	---	---
983	992	1001	1010	1019	1028
TAT GGA TGA	ATA GAT AGA	TGG TGT TGG	CAT GTA AAT	TGC AGA GAA	AAC AAA ACC
---	---	---	---	---	---
1037	1046	1055	1064	1073	1082
AAA GCT GAT	TGG AAA CAA	TTA ATT GTG	GGT GTC TGA	GGG GGA AGG	TCG CAG CTT
---	---	---	---	---	---

FIGURE 2C

[illegible]

12 of 21

5' CAA CCA GGG TCA GGC TGT GCT CAC CAC AGT TTC CTC TGG CGG CAT GTA AAG GCT CCA

5'	CAA	CCA	GGG	TCA	GGC	TGT	GCT	CAC	CAC	AGT	TTC	CTC	TGG	CGG	CAT	GTA	AAG	GCT	CCA
	9				18		27						36			45			54
	CAA	AGG	AGT	TGG	GAG	TTC	AAA	TGA	GGC	TGC	TGC	GGA	CGG	CCT	GAG	GAT	GGA	CCC	
	63				72		81						90			99			108
	CAA	CTG	GAC	CTG	CCG	AGC	GTG	GCA	CTG	AGG	CAG	CGG	CTG	ACG	CTA	CTG	TGA		
	117				126		135						144			153			162
	CAA	GCC	CTG	GAC	CTG	CCC	AGC	GTG	GCA	CTG	AGG	CAG	CGG	CTG	ACG	CTA	CTG	TGA	
	171				180		189						198			207			216
	GGG	AAA	GAA	GGT	TGT	GAG	CAG	CCC	CGC	AGG	ACC	CCT	GGC	CAG	CCC	TGG	CCC	CAG	
	225				234		243						252			261			270
	CCT	CTG	CCG	GAG	CCC	TCT	GTG	GAG	GCA	GAG	CCA	GTG	GAG	CCC	AGT	GAG	GCA	GGG	
	279				288		297						306			315			324
	CTG	CTT	GGC	AGC	CAC	CGG	CCT	GCA	ACT	CAG	GAA	CCC	CTC	CAG	AGG	CCA	TGG	ACA	
	333				342		351						360			369			378
	GGC	TGC	CCC	GCT	GAC	GGC	CAG	GGT	GAA	GCA	TGT	GAG	GAG	CCG	CCC	CGG	AGC	CAA	

FIGURE 3A

13 g21

387		396			405			414			423			432			
GCA	GGA	GGG	AAG	AGG	CTT	TCA	TAG	ATT	CTA	TTC	ACA	AAG	AAT	AAC	CAC	CAT	TTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
441		450		459		468		477		486		486		486		486	
GCA	AGG	ACC	ATG	AGG	CCA	CTG	TGC	GTG	ACA	TGC	TGG	TGG	CTC	GGA	CTG	CTG	GCT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M		R	P	L	C	V	T	C	W	L	G	L	L	A	A	A	A
495		504		513		522		531		540		540		540		540	
GCC	ATG	GGA	GCT	GTT	GCA	GGC	CAG	GAG	GAC	GGT	TTT	GAG	GGC	ACT	GAG	GAG	GGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	M	G	A	V	A	G	Q	E	D	G	F	E	G	T	E	E	G
549		558		567		576		585		594		594		594		594	
TCG	CCA	AGA	GAG	TTC	ATT	TAC	CTA	AAC	AGG	TAC	AAG	CGG	GCG	GGC	GAG	TCC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	P	R	E	F	I	Y	L	N	R	Y	K	R	A	G	E	S	Q
603		612		621		630		639		648		648		648		648	
GAC	AAG	TGC	ACC	TAC	ACC	TTC	ATT	GTG	CCC	CAG	CAG	CGG	GTC	ACG	GGT	GCC	ATC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	K	C	T	Y	T	F	I	V	P	Q	Q	R	V	T	G	A	I
657		666		675		684		693		702		702		702		702	
TGC	GTC	AAC	TCC	AAG	GAG	CCT	GAG	GTG	CTT	CTG	GAG	AAC	CGA	GTG	CAT	AAG	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
C	V	N	S	K	E	P	E	V	L	L	E	N	R	V	H	K	Q

FIGURE 3B

14 of 21

15 of 21

711	720	729	738	747	756
GAG CTA GAG CTG CTC AAC AAT GAG CTG CTC AAG CAG AAG CAG ATC GAG ACG					
E L E L L N N E E L L L K Q K R Q I E T					
765	774	783	792	801	810
CTG CAG CAG CTG GTG GAG GTG GAC GGC GGC ATT GTG AGC GAG GTG AAG CTG CTG					
L Q Q L V E V D G G I V S E V K L L					
819	828	837	846	855	864
CGC AAG GAG AGC CGC AAC ATG AAC TCG CGG GTC ACG CAG CTC TAC ATG CAG CTC					
R K E S R N M N S R V T Q L Y M Q L					
873	882	891	900	909	918
CTG CAC GAG ATC ATC CGC AAG CGG GAC AAC GCG TTG GAG CTC TCC CAG CTG GAG					
L H E I I R K R D N A L E L S Q L E					
927	936	945	954	963	972
AAC AGG ATC CTG AAC CAG ACA GCC GAC ATG CTG CAG CTG GCC AGC AAG TAC AAG					
N R I L L N Q T A D M L Q L A S K Y K					
981	990	999	1008	1017	1026
GAC CTG GAG CAC AAG TAC CAG CAC CTG GCC ACA CTG GCC CAC AAC CAA TCA GAG					
D L E H H K Y Q H L A A T L A H N Q S E					

FIGURE 3C

16 g21

.....  
if it shall and the if it  
if it shall and the if it  
.....

1035	1044	1053	1062	1071	1080
ATC ATC GCG CAG CTT GAG GAG CAC TGC CAG AGG GTG CCC TCG GCC AGG CCC GTC					
I I A Q L E E H C Q R V P S A R P V					
1089	1098	1107	1116	1125	1134
CCC CAG CCA CCC CCC GCT GCC CCG CCC CGG GTC TAC CAA CCA CCC ACC TAC AAC					
P Q P P P A A P P R V Y Q P P T Y N					
1143	1152	1161	1170	1179	1188
CGC ATC ATC AAC CAG ATC TCT ACC AAC GAG ATC CAG AGT GAC CAG AAC CTG AAG					
R I I N Q I S T N E I Q S D Q N L K					
1197	1206	1215	1224	1233	1242
GTG CTG CCA CCC CCT CTG CCC ACT ATG CCC ACT CTC ACC AGC CTC CCA TCT TCC					
V L P P P L P T M P T L T S L P S S					
1251	1260	1269	1278	1287	1296
ACC GAC AAG CCG TCG GGC CCA TGG AGA GAC TGC CTG CAG GCC CTG GAG GAT GGC					
T D K P S G P W R D C L Q A L E D G					
1305	1314	1323	1332	1341	1350
CAC GAC ACC AGC TCC ATC TAC CTG GTG AAG CCG GAG AAC ACC AAC CGC CTC ATG					
H D T S S I Y L V K P E N T N R L M					

FIGURE 3D



1359	1368	1377	1386	1395	1404
CAG GTG TGG TGC GAC CAG AGA CAC GAC CCC GGG GGC TGG ACC GTC ATC CAG AGA					
Q V W C D Q R H D P G G W T V I Q R					
1413	1422	1431	1440	1449	1458
CGC CTG GAT GGC TCT GTT AAC TTC TTC AGG AAC TGG GAG ACG TAC AAG CAA GGG					
R L D G S V N F F R N W E T Y K Q G					
1467	1476	1485	1494	1503	1512
TTT GGG AAC ATT GAT GGC GAA TAC TGG CTG GGC CTG GAG AAC ATT TAC TGG CTG					
F G N I D G E Y W L G L E N I Y W L					
1521	1530	1539	1548	1557	1566
ACG AAC CAA GGC AAC TAC AAA CTC CTG GTG ACC ATG GAG GAC TGG TCC GGC CGC					
T N Q G N Y K L L L V T M E D W S G R					
1575	1584	1593	1602	1611	1620
AAA GTC TTT GCA GAA TAC GCC AGT TTC CGC CTG GAA CCT GAG AGC GAG TAT TAT					
K V F A E Y A S F R L E P E S E Y Y					
1629	1638	1647	1656	1665	1674
AAG CTG CGG CTG GGC TAC CAT GGC AAT GCG GGT GAC TCC TTT ACA TGG CAC					
K L R L G R Y H G N A G D S F T W H					

FIGURE 3E

..... if it equal and the if it  
if it equal and the if it  
..... if it equal and the if it

1683	1692	1701	1710	1719	1728
AAC GGC AAG CAG TTC ACC ACC CTG GAC AGA GAT CAT GAT GTC TAC ACA GGA AAC					
N G K Q F T T L D R D H D V Y T G N					
1737	1746	1755	1764	1773	1782
TGT GCC CAC TAC CAG AAG GGA GGC TGG TGG TAT AAC GCC TGT GCC CAC TCC AAC					
C A H Y Q K G G G W W Y N A C A H S N					
1791	1800	1809	1818	1827	1836
CTC AAC GGC GTC TGG TAC CGC GGC GGC CAT TAC CGG AGC CGC TAC CAG GAC GGA					
L N G V W Y R G G H Y R S R Y Q D G					
1845	1854	1863	1872	1881	1890
GTC TAC TGG GCT GAG TTC CGA GGA GGC TCT TAC TCA CTC AAG AAA GTG GTG ATG					
V Y W A E F R G G S Y S L K K V M					
1899	1908	1917	1926	1935	1944
ATG ATC CGA CCG AAC CCC AAC ACC TTC CAC TAA GCC AGC TCC CCC TCC TGA CCT					
M I R P N P N T F H *					
1953	1962	1971	1980	1989	1998
CTC GTG GCC ATT GCC AGG AGC CCA CCC TGG TCA CGC TGG CCA CAG CAC AAA GAA					

FIGURE 3F

[illegible]

19 y 21

20 y 21

## NORTHERN ANALYSIS OF SEQ ID NO:3

Category	cDNAs	Libraries	Abund	%Abund
Cardiovascular	270162	15/72	19	0.0070
Connective	147886	15/54	26	0.0176
Digestive	514430	33/151	54	0.0105
Embryonic	107325	2/23	2	0.0019
Endocrine	233587	7/63	8	0.0034
Exocrine	255105	17/64	28	0.0110
Female Reprod	445078	25/113	48	0.0108
Male Reprod	453150	32/118	44	0.0097
Germ Cells	46185	1/5	9	0.0195
Hemic/Immune	701709	8/166	8	0.0011
Liver	110945	2/34	2	0.0018
Musculoskeletal	162794	10/50	16	0.0098
Nervous	973795	25/221	45	0.0046
Pancreas	111757	3/25	19	0.0170
Respiratory	407942	14/95	21	0.0051
Sense Organs	25346	1/10	1	0.0039
Skin	72110	1/15	1	0.0014
Stomatognathic	14025	0/11	0	0.0000
Unclass./Mixed	150146	6/19	31	0.0206
Urinary Tract	287931	12/66	22	0.0076
Totals	5491408	229/1375	404	0.0001

Legend: The first column presents the category (cell tissue or organ), the second column, the number of cDNAs sequenced for that category; the third column, description of the tissue; the fourth column, absolute abundance of the transcript; and the fifth column, percent abundance of the transcript (abundance divided by the number of clones)

FIGURE 4

21 y 21

# Differential Expression of SEQ ID NO:3 in Pancreas

Found in:

<u>Library</u>	<u>cDNAs</u>	<u>Description</u>	<u>Abund</u>	<u>%Abund</u>
PANCTUP01	1205	pancreatic tumor, TIGR	1	0.0830
PANCTUP032	2651	pancreas tumor, adenoCA, 3' CGAP	17	0.0751
PANCTUT021	1545	pancreatic tumor, anaplastic CA, 45F	1	0.0087

Not found in:

<u>Library</u>	<u>cDNAs</u>	<u>Description</u>
PANCDIR02	2023	pancreas, type I diabetes, 43F, RP
PANCDIT01	1741	pancreas, type I diabetes, 15M
PANCN0T23	3919	pancreas, type I diabetes, 43F
PANCDIT03	688	pancreas, type II diabetes, 57M
PANCNOE02	2834	pancreas, 8M, 5RP
PANCNOP03	589	pancreas, 34F, WN
PANCNOP05	373	pancreas, CGAP
PANCN0T01	4452	pancreas, 29M
PANCN0T0411135		pancreas, 5M
PANCN0T05	6788	pancreas, 2M
PANCN0T07	6991	pancreas, fetal, 23wM
PANCN0T08	3901	pancreas, pancreatitis, mw/adenoCA, 65F, m/PANCTUT01
PANCN0T15	3638	pancreas, islet cell hyperplasia, 15M
PANCN0T16	2994	pancreas, aw/Patau's, fetal, 20wM
PANCN0T17	4034	pancreas, mw/neuroendocrine CA, aw/node, liver mets, 65F
PANCN0T19	3772	pancreas, 8M
PANCN0T21	3841	pancreas, 8M
PANCN0T22	1356	pancreas, 17F

Legend: The first range shows the expression of SEQ ID NO:3 in pancreas. SEQ ID NO:3 is differentially expressed in pancreatic tumors and diagnostic of that condition. The second range shows that the sequence is not expressed in type I and II diabetes, in pancreatitis, or in metastatic liver cancer.

Where present, the first column presents the library name, the second column, the number of cDNAs sequenced for that library; the third column, description of the tissue; the fourth column, absolute abundance of the transcript; and the fifth column, percent abundance of the transcript (abundance divided by the number of clones)

Note: Normalized and subtracted tissues, which have high abundance transcripts removed before sequencing, were not considered in this analysis.

FIGURE 5